# Maternal line genetic influence on fresh pork quality and palatability

Thesis

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**Abstract**

The present experiment was conducted to characterize the influence of maternal genetics on tenderness and fresh meat quality of the *longissimus dorsi* muscle (LM). Three sets of littermate barrows and gilts, sired by a single Berkshire boar (n = 4 Berkshire × Berkshire female, BB; n = 5 Berkshire × Landrace female, BL; and n = 5 Berkshire × Saddleback/Berkshire female, BS) were reared in a common contemporary group to a target BW of 105 kg, transported to The Ohio State University Meat Science Laboratory abattoir, and rested for 15 h with free access to water prior to harvest. At 24 h post harvest, backfat depth (BF), loin muscle area (LMA) and loin quality measurements (ultimate pH, visual marbling, wetness, firmness and color, and objective Minolta L*, a*, and b*) were measured on the $10^{th}$- and $11^{th}$-rib loin surface .A loin section, posterior to the $10^{th}$ and $11^{th}$ rib carcass split, was removed from the right side of the carcass at 24 h post harvest, aged for 7 d and used to measure LM Warner-Bratzler shear force (WBSF) and intramuscular fat (IMF) content. Maternal line had no effect ($P > 0.10$) on BF, LMA, visual marbling, firmness and color, L*, a*, b* values or IMF; however, maternal line did influence WBSF ($P < 0.01$), whereby BB and BL genetic lines produced LM with lesser, more desirable WBSF when compared with LM from BL pigs, with a trend for . with greater pH improved LM firmness. Electrophoretic profiles of the myofibrillar and sarcoplasmic protein fractions identified banding pattern variation that may explain variation in WBSF across the genetic lines. The results from the present study suggest that maternal genetic lines containing Berkshire and Berkshire/Saddleback breeds

produced carcasses with similar composition as the Landrace maternal line and, in addition, provided a pork product (LM) with greater water-holding capacity (greater pH) and improved tenderness (WBSF).

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## Introduction

The term meat quality has come to incorporate characteristics including composition of the carcass, appearance, eating quality, wholesomeness, and nutritional value of the product. Meat quality, as defined by consumers, is composed of several attributes related to eating characteristics. A consumer's eating satisfaction, or palatability, of the meat product is often a primary factor in purchase and repeat purchase decisions. Eating satisfaction relies on several factors including tenderness, juiciness and flavor (Tarrant, 1998; Bindon and Jones, 2001); however, tenderness has been shown to have the greatest effect on a consumer's perception of palatability (Savell et al., 1987; Savell et al., 1989).

Tenderness of meat can be influenced by genetics, the environment in which the animal was raised, husbandry practices, transportation conditions, lairage, and harvesting procedures. Stunning method and early postmortem factors influencing conversion of muscle to meat, such as the time from stun to chill and rate of carcass chill, have been shown to influence meat quality. In addition, carcass or cut ageing period, methods of packaging and final preparation technique will also influence the resulting tenderness of a meat product. Breed differences have been reported for many characteristics that influence pig growth rate, carcass composition, and meat quality. In addition, mutant Porcine Stress Syndrome and Rendement Napole genotypes have been identified and reported to have negative effects on carcass and meat quality characteristics (Goodwin, 2004).

Two studies conducted at the Ohio Agriculture Research and Development Center, Western Research Station have shown that Berkshire pigs consistently produce more tender pork loin chops when compared to chops derived from Landrace pigs (Still, 2005; Naber, 2007). Still et al. (2005) reported that tenderness in pork chops from Berkshire and Landrace pigs improved at relatively the same rate during the postmortem ageing period; however, pork chops from Berkshire pigs were more tender throughout the ageing period (Figure 1). Naber (2007) reported that purebred Berkshire pigs, when compared with Berkshire × Landrace or Landrace × Berkshire pigs, produced more tender pork chops (Figure 2). Of note, in both studies, pigs having a Landrace genetic influence produced larger, heavier muscled pigs and carcasses with greater carcass value when compared with contemporary purebred Berkshire pigs.

One of the main trends in the pork industry over the past few years has been to increase carcass weights, resulting in a net improvement of the economic efficiency for the pork packing and processing sectors due to a greater volume of pork produced for an equal investment in plant labor and facilities. Thus, there has been greater selection pressure placed on reducing backfat and increasing the rate of muscle growth, which in turn maintains a high percent lean in the heavier pork carcasses. However, emphasis on an increased rate of lean growth may have indirectly resulted in selection for genes that negatively impact pork product tenderness. Tougher meat and the subsequent decrease in palatability may result in decreased pork demand and fewer repeat purchases. The present experiment was a pilot study conducted to investigate the influence of the maternal line genetic contribution to progeny's pork loin tenderness and fresh pork quality attributes.

**Materials and methods**

*Animals*

Three sets of littermate barrows and gilts, sired by a single Berkshire boar (n = 4 Berkshire × Berkshire female, BB; n = 5 Berkshire × Landrace female, BL; and n = 5 Berkshire × Saddleback/Berkshire female, BS) were reared in a common contemporary group at the Ohio Agriculture Research and Development Center, Western Research Station, South Charleston, Ohio. Pigs were housed in a finishing facility with partially slotted-floors, provided a minimum of 0.80 $m^2$ • $pig^{-1}$ space allocation, and provided ad libitum access to standard finishing diets fed in three phases. Pigs were taken off test at a targeted BW of 105 kg, transported to The Ohio State University Meat Science Laboratory abattoir, and rested for 15 h with free access to water. Pigs were harvested following USDA-approved stunning procedures and all procedures were performed under federal inspection.

*Carcass Measurements*

At 24 h post harvest the left side of the carcass was split between the 10th and 11th ribs. Tenth rib backfat depth (BF) and loin muscle area (LMA) were measured on the hanging carcass and loin quality measurements were assessed following procedures outlined in Composition and Quality Assessment Procedures (NPPC, 2000). Ultimate loin pH was measured at approximately one centimeter below the exposed $10^{th}$ rib loin surface. Following a 30 minute bloom, visual loin muscle firmness and wetness scores were recorded on a 1 to 3 subjective scale according to procedures outlined by NPPC (2000). Loin muscle color (Minolta L*, a*, and b*) was objectively measured on the $10^{th}$- and $11^{th}$-rib loin surface using a Model CR-410 Minolta Chroma Meter (Minolta

Corp, Ramsey, NJ) fitted with a 50 mm diameter orifice and using a D65 illuminant standardized against a white tile.

A loin (LM) section, located posterior to the $10^{th}$ and$11^{th}$ rib split, was removed from the right side of the carcass at 24 h post harvest and three, 5.08-cm thick, bone-in LM chops were cut, vacuum packaged, aged for 7 d, and subsequently frozen at -20º C until used in the measurement of Warner-Bratzler shear force (WBSF) and intramuscular fat (IMF) percentage by ether extraction (AOAC, 1984). Prior to cooking, the ends of the frozen loin sections were cut on a bandsaw to obtain a standard 2.54-cm thick chop that was then allowed to thaw at 2 ºC, deboned, and defatted. Chops were cooked on a clam-style electric grill at 190° C (George Foreman grilling machine, Lake Forest, IL) until chops reached an internal temperature of 71°C. Loin chop temperatures were monitored using a hand-held thermocouple (Ashcroft, AFTX 392 SKW, Stratford, CT). After reaching their cooked temperature, chops were allowed to cool to room temperature. Four, 1.27-cm diameter cores were taken from each chop parallel to the muscle fiber orientation and WBSF was measured on each muscle core using a TA.XT2 Texture Analyzer (Texture Technologies, Scarsdale, New York) equipped with a WBSF probe. In the statistical analysis, the average WBSF for the four cores reported.

*Proteomic Analysis*

To obtain the sarcoplasmic and myofibrillar protein fractions from each LM sample, 250 mg of muscle tissue from each sample was homogenized (OMNI International; Marietta, GA.) at full speed in 2 ml of cold rigor buffer [10 mM Trismaleate, 60 mM KCl, 5 mM $MgCl_2$, 1 mM EGTA, 0.4 mM Pefabloc SC Plus, (Boehringer Mannheim Corp., Indianapolis, IN), pH 6.8] on ice. The homogenate was

centrifuged at 10,000 ×g for 10 min at 4 °C and the supernatant were collected and re-centrifuged a second time under the same conditions. The supernatant obtained after the second centrifugation step was designated as the sarcoplasmic fraction. The initial pellet was washed two more times by re-suspending the pellet in fresh cold rigor buffer, centrifuged again at 10,000 ×g for 10 min at 4 °C and the supernatant was discarded. The pellet obtained after the last wash was designated as the myofibrillar fraction. After discarding the supernatant on the last wash, only 75 mg of pellet were kept in the tube and they were dissolved in 1.5 ml of sample buffer (8 M urea / 2 M thiourea, 75 mM DTT, 50 mM Tris, 3% SDS, 0.004% bromophenol blue, pH 6.8) and incubated on ice for 30 min. Five hundred microliters of the sarcoplasmic fraction were thoroughly mixed with one milliliter of sample buffer and incubated on ice for 30 min. For the one dimensional electrophoretic separation, samples were centrifuged again at 10,000 ×g for 10 min at room temperature before loading into a 1 mm × 12 cm ×14 cm discontinuous polyacrylamide slab gel consisting of a 10% resolving gel [30:0.8, acrylamide/N,N0-bis(methylene acrylamide)] and a 3% stacking gel. Electrophoretic separation was carried out at a constant voltage of 10 $Vcm^{-1}$. Following electrophoretic separation, the gels were imaged and analyzed as described below (Zapata et al., 2009) on a Typhoon 9410 laser scanner (GE Healthcare, Chalfont St. Giles, U.K.). Digital images were analyzed using the Total Lab TL120 (Nonlinear Dynamics Inc., Newcastle upon Tyne, U.K.) software.

*Statistical Analysis*

Effects of maternal genetic line on carcass, fresh meat quality, and cooked meat quality attributes were analyzed as dependent variables using General Linear Models

(GLM) of SAS (SAS v.9.2, SAS Institute Inc., Cary, NC). Maternal genetic line was the only fixed effect used in the model and least squares means were separated using the DIFF option. Temperature of the cooked LM was used as a linear covariate to more appropriately assess maternal line influences on WBSF and cooking loss. Correlation analyses were performed using the PROC CORR procedures in SAS to estimate relationships among traits.

The statistical analysis on the gels was performed using a mixed model to estimate the mean band percentage values and mean band percentage differences across maternal genetic lines. Maternal genetic line was considered a fixed effect. All estimates were obtained per band. The model is:

$$\text{Band percentage}_{ijk} = \text{Band}_i \mid \text{Genetic line}_j + \varepsilon_{ijk}$$

where Band percentage$_{ijk}$ is the dependent variable measured on the $i^{th}$ band of the $j^{th}$ genetic line from the $l^{th}$ animal; Band$_i$ is the effect of the $i^{th}$ electrophoretically-resolved band matched across lanes and gels in the image analysis software (i = 1, ..., band n); **Genetic Line$_j$** is the effect of the $j^{th}$ maternal genetic line (j = Berkshire ×Berkshire, Berkshire × Berkshire/Saddleback, Berkshire × Landrace); $\boldsymbol{\varepsilon_{ijkl}}$ is the random error inherent to each measurement, which is assumed to be independent of other observations and normally distributed with mean zero. Significance was declared at a 95% confidence level.

**Results and Discussion**

The least squares means for carcass and loin muscle quality traits by genetic type can be found in Table 1. Maternal genetic line had no effect ($P > 0.10$) on BF, LMA, or lean content, indicating that the maternal line genetics tested are expected to have similar carcass value. Fresh quality indicators, including loin pH, visual marbling, visual color, objective color (L*), and IMF were not different across the maternal genetic lines. However, the maternal influence of Berkshire and Berkshire × Saddleback genetics improved ($P < 0.01$) tenderness (lower WBSF) when compared to LM from Landrace females (6.73, 5.96, and 11.44 lb, respectively). These results indicate that Berkshire maternal characteristics alone or in combination with Saddleback maternal genetics improved LM tenderness. Conversely, the results indicate that the Landrace maternal genetic component appears to override the Berkshire-sire genetic influence for tenderness measurements. The findings that support superior meat quality in purebred Berkshire pigs are further supported by the work of Still (2005) and Naber (2007).

Image and statistical analyses of the 1- D electrophoresis assessments revealed differences ($P < 0.05$) in banding patterns in both the sarcoplasmic and myofibrillar muscle fractions when compared among the maternal genetic lines (Figures 3 and 4). One sarcoplasmic fraction (b15) and three myofibrillar (b2, b8, b9) banding patterns were different across the maternal genetic lines. While these banding patterns differ, the association of these bands with specific quality attributes, specific proteins, and the cause of variation at these locations is still under investigation.

The results of this pilot study suggest Berkshire and Saddleback maternal genetics may be considered viable genetic options for developing commercial female lines that

contribute to improved fresh pork quality without negatively impacting carcass composition. Band differences on the gels indicate that there are protein differences among the breeds; however, further sequencing is needed to determine which proteins are different. Determination of the relationship of identified protein fractions with causal variation in fresh pork quality may lead to identification of gene or gene expression differences between individual animals and across breeds. Ultimately, this study warrants larger scale studies to confirm the observed maternal line impact on pork quality and palatability.

## Conclusion

In modern times, there are no real time indicators of pork quality to reward producers for supplying high quality, tender products. However, by establishing breeds that bring forth production efficiency without sacrificing quality may benefit producers and provide an avenue to receive premiums on the bottom line. The Berkshire breed may be capable of producing high-quality cuts without negatively impacting carcass cutability during the finishing phase. Protein differences were observed between Berkshire and Landrace breeds, but need further investigation to conclude which proteins are different and what is causing changes amongst the proteins and how they ultimately influence meat quality.

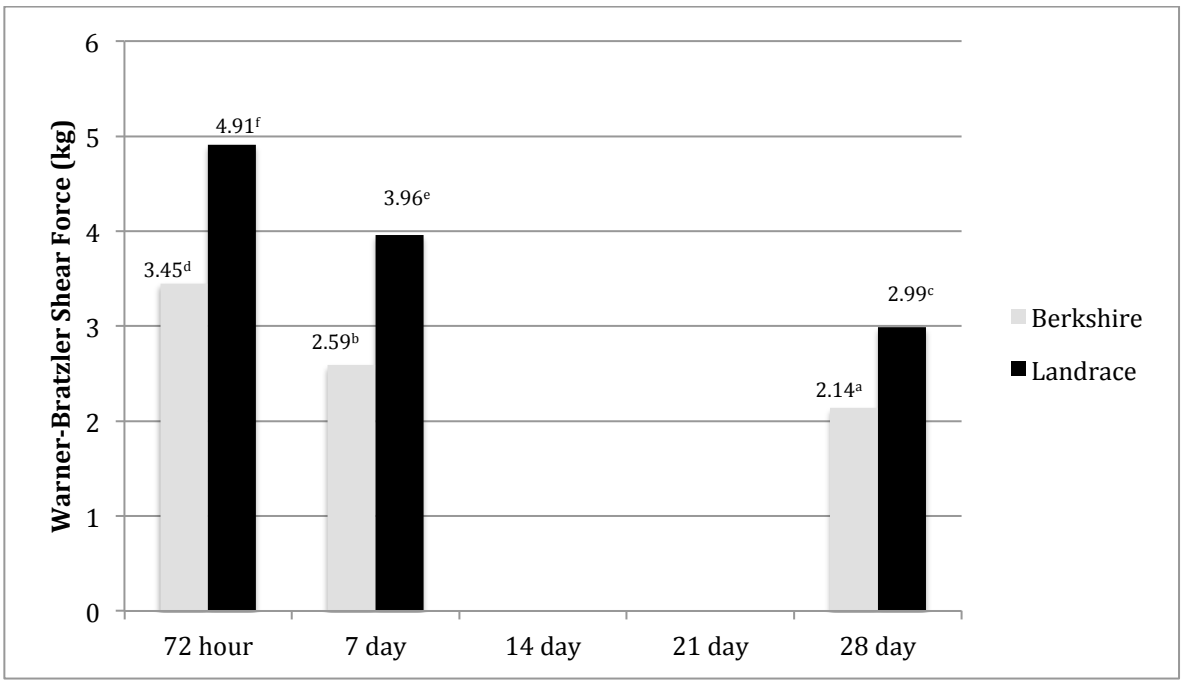


Figure 1. Warner Bratzler Shear Force for pork chops from purebred Berkshire, Purebred Landrace during postmortem aging (adapted from Still, 2005).

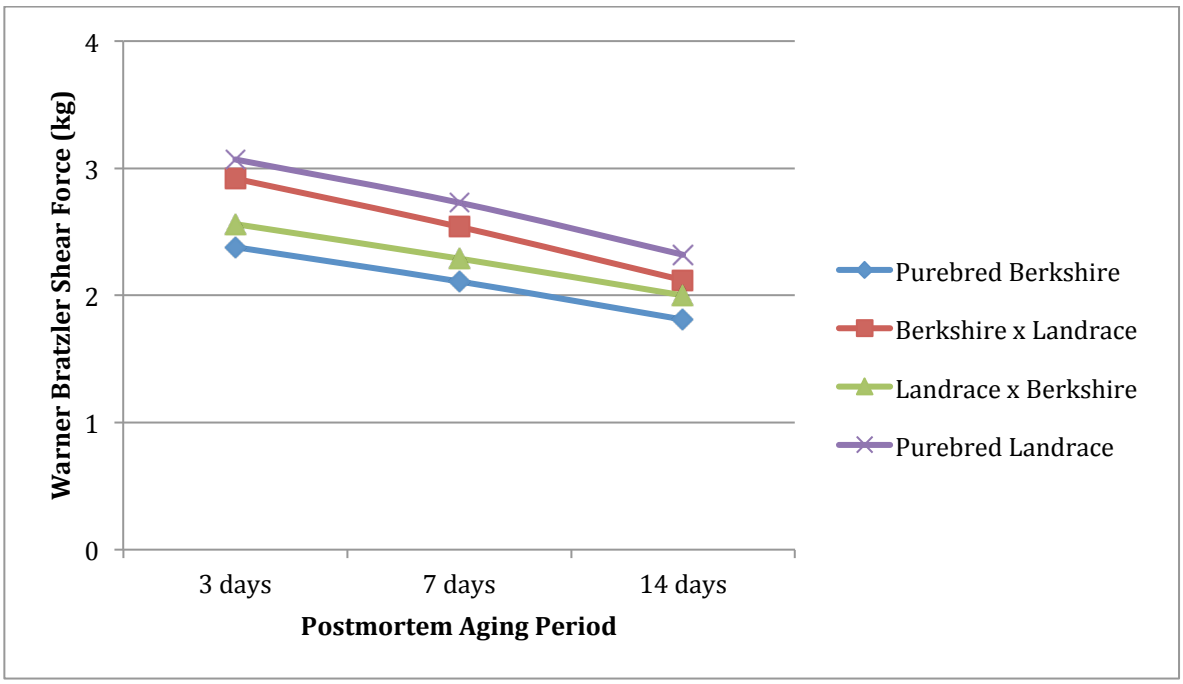


Figure 2. Warner Bratzler Shear Force for pork chops from purebred Berkshire, Purebred Landrace, and their reciprocal crosses during 14 days postmortem aging (adapted from Naber, 2007).

| Berkshire Sire × Maternal Genetic Line | N | Carcass and Meat Quality Traits | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | Backfat (in) | Loin Muscle Area ($in^2$) | Percent Lean (%) | Loin Color | Minolta L* | Marbling | IMF (%) | pH | WBSF (lb) |
| Berkshire | 4 | 1.10 | 5.22 | 46.7 | 3.0 | 55.2 | 1.6 | 1.49 | 5.65 | 6.73[a] |
| Berkshire × Saddleback | 5 | 0.97 | 5.46 | 48.7 | 3.2 | 53.1 | 2.0 | 1.56 | 5.69 | 5.96[a] |
| Landrace | 5 | 0.93 | 5.40 | 49.3 | 3.0 | 54.0 | 2.0 | 1.11 | 5.55 | 11.44[b] |
| Pooled Std Error | | ± 0.08 | ± 0.24 | ± 1.2 | ± 0.3 | ± 1.1 | ± 0.2 | ± 0.20 | ± 0.04 | ± 1.00 |
| Significance | | NS | NS | NS | NS | NS | NS | NS | $P = 0.12$ | $P < 0.01$ |

[ab]Means within a column without a common superscript differ ($P < 0.05$)

NS = Not Significant ($P > 0.05$)

Table1. Least squares means and standard errors for carcass and meat quality traits of loins derived from three maternal genetic lines of pigs.

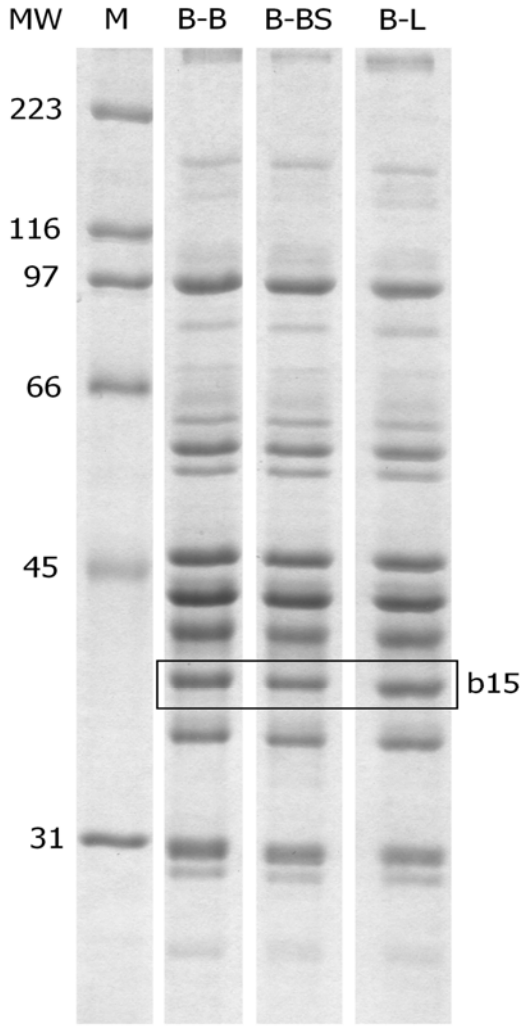


Figure 3. Sarcoplasmic fraction

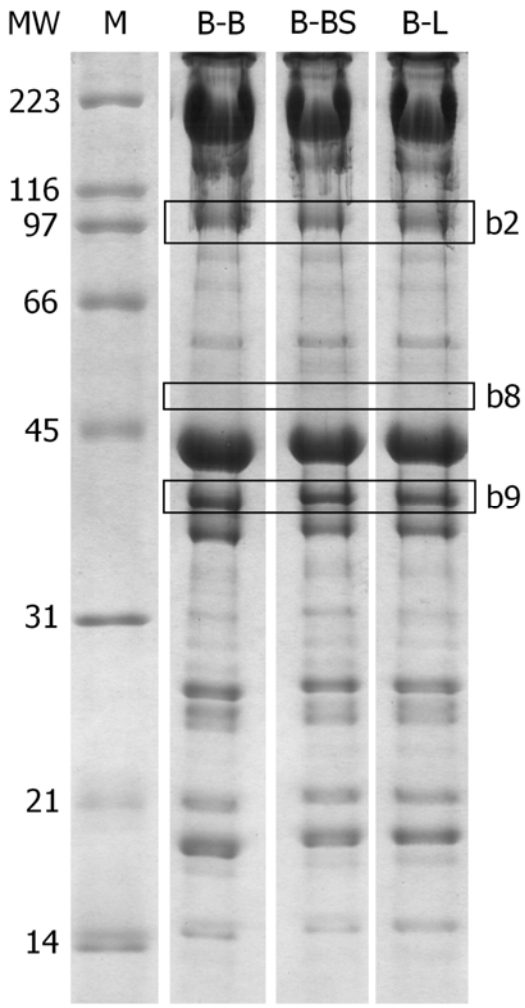


Figure 4. Myofibrillar fraction

Figures 4 and 5. 1-D electrophoretic profiles of myofibrillar (Figure 4) and sarcoplasmic (Figure 3) fractions of *Longissimus dorsi* muscle measured at 7 d postmortem. Samples derived from purebred Berkshire (B-B), Berkshire sire × Berkshire/Saddleback (B-BS) female, and Berkshire sire × Landrace (B-L) female genetic types. Boxes indicate bands that are significantly different across genetic types.

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